

SEQUENCE LISTING



<110> JENTSCH, Thomas J.

<120> NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
POTASSIUM CHANNELS

<130> 2815-1278

<140>

<141>

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 2335

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2335)

<220>

<221> CDS

<222> (33)..(2170)

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Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
1 5 10

ctg ggt ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc 160
Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
15 20 25

acg gcc gtg cag agc gaa cag gcc gag gcg gcc ggg gcc gcc tcc ccg 208
Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Ser Pro
30 35 40

cgc cgc ctc gcc ctc ctg gcc agc ccc ctg ccg ccg gcc gcg ccc ctc 256
Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
45 50 55

act ggg cag gag tac aac tac aac tac gaa tga gaa cag tga tac	114
Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser	
60 65 70	
gac gag cac aag agc tac cgc cgc ctg cag aac tgg gtc tac aac gtc	352
Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val	
75 80 85 90	
ctg gag cgg ccc cgc ggc tgg gcc ttc gtc tac cac gtc ttc ata ttc	401
Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe	
95 100 105	
ttg ctg gtc ttc agc tgc ctg gtc ctg tct gtc ctg tcc act atc cag	448
Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln	
110 115 120	
gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtc	496
Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val	
125 130 135	
atg atc gtc gtt ttc gcc ttg gag tac atc gtc cgg gtc tgg tcc gcc	544
Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala	
140 145 150	
gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc	592
Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala	
155 160 165 170	
aga aag ccc ttc tgt gtc atc gac ttc atc gtc ttc gtc gcc tcg gtc	640
Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val	
175 180 185	
gcc gtc atc gcc ggc ggt acc cag gcc aac atc ttc gcc acg tcc gcg	688
Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala	
190 195 200	
ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtc cgc atg gac	736
Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp	
205 210 215	
cgc cgc ggc ggc acc tgg aag ctg ctg gcc tca gtc gtc tac gcg cat	784
Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His	
220 225 230	
agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtc ctc atc	832
Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile	
235 240 245 250	

ttc gac ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc	971
Phe Ala Ser Phe Leu Val Tyr Leu Ala Ala Lys Asp Ala Asn Ser Asp	
288 289 290	
ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc	972
Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr	
271 272 273 274 275 276 277 278 279 280	
acc atc ggc tac ggt gac aag aca cgc cac aca tgg ctg ggc agg gtc	973
Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val	
283 284 285 286 287 288 289 290 291 292 293 294	
ctg gct gct ggc ttc ggc tta ctg ggc atc tat ttc ttt gac ctg cct	1024
Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro	
300 301 302 303 304 305 306 307 308 309 310 311	
gac ggc atc cta ggc tcc ggc ttt ggc ctg aag gtc cag gag cag cac	1072
Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His	
315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330	
cgg cag aag cac ttc gag aag cgg agg atg cgc gca gcc aac ctg atc	1120
Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile	
333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348	
cag gct gcc tgg cgc ctg tac tcc acc gat atg agc cgg gcc tac ctg	1168
Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu	
350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365	
aca gcc acc tgc tac tac tat gac agt atc ctg cca tcc ttc aga gag	1216
Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu	
366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381	
ctg gcc ctg ttg ttt gag cac gtg caa cgg gcc cgc aat ggg ggc cta	1264
Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu	
382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397	
cgg ccc ctg gag gtg cgg cgg ggc cgc gta ccc gac gga gca ccc tcc	1312
Arg Pro Leu Gln Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser	
398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	
cgt tac cgc ccc gtt gcc acc tgc cac cgg cgc ggc agc acc tcc ttc	1360
Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe	
414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429	
tgc cct ggg gaa agc agc cgg atg ggc atc aaa gac cgc atc cgc atg	1408
Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met	
430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445	

ttt aag ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt	1460
Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro	
445 480 485	
cca aca atg ccc acc tcc cca agc agc gag cag gtg ggt gag gcc acc	1504
Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Gln Ala Thr	
460 465 470	
agc ccc acc aag gtg caa aag agc tgg agc ttc aat gac cgc acc cgc	1552
Ser Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg	
475 480 485 490	
ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc	1600
Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala	
495 500 505	
ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg	1648
Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr	
510 515 520	
gtg gac gac atc atg cct gct gtg aag aca gtc atc cgc tcc atc agg	1696
Val Asp Asp Ile Met Pro Ala Val Lys Thr Val Ile Arg Ser Ile Arg	
525 530 535	
att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga	1744
Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg	
540 545 550	
cgc tac gac gtg aag gac gtc att gag cag tac tca gca ggc cac ctg	1792
Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu	
555 560 565 570	
gac atg ctg ggc cgg atc aag agc ctg caa act cgg gtg gac caa att	1840
Asp Met Leu Gly Arg Ile Lys Ser Leu Gln Thr Arg Val Asp Gln Ile	
575 580 585	
gtg ggt cgg ggg ccc ggg gac agg aag gcc cgg gag aag ggc gac aag	1888
Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys	
590 595 600	
ggg ccc tcc gac gog gag gtg gtg gat gaa atc agc atg atg gga cgc	1936
Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg	
605 610 615	
gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac	1984
Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp	
620 625 630	

635 640 645 650
 Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala
 635 640 645 650

655 660 665
 Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser
 655 660 665

670 675 680
 Asp Tyr His Ser Pro Val Asp His Gln Asp Ile Ser Val Ser Ala Gln
 670 675 680

685 690 695
 Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp
 685 690 695

2230
 gggaattctc agaggcaggg cagcacacgg ccagcccccgc ggccctgggcgc tcgcactgcc

2290
 ctctgaggcc tcggactcc tctcgtactt gaactcactc cctcacgggg agagagacca

2335
 caagcagtat tgagctgcct gactgggcgt ggtacctgct gtggg

4210: 2

4211: 695

4212: PRT

4213: Homo sapiens

4400: 2

Met	Ala	Glu	Ala	Pro	Pro	Arg	Arg	Leu	Gly	Leu	Gly	Pro	Pro	Pro	Gly
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Asp	Ala	Pro	Arg	Ala	Glu	Leu	Val	Ala	Leu	Thr	Ala	Val	Gln	Ser	Glu
			20					25				30			
Gln	Gly	Glu	Ala	Gly	Gly	Gly	Gly	Ser	Pro	Arg	Arg	Leu	Gly	Leu	Leu
		35					40					45			
Gly	Ser	Pro	Leu	Pro	Pro	Gly	Ala	Pro	Leu	Pro	Gly	Pro	Gly	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Ala	Cys	Gly	Gln	Arg	Ser	Ser	Ala	Ala	His	Lys	Arg	Tyr
65				70				75				80			
Arg	Arg	Leu	Gln	Asn	Trp	Val	Tyr	Asn	Val	Leu	Glu	Arg	Pro	Arg	Gly
			85					90				95			
Trp	Ala	Phe	Val	Tyr	His	Val	Phe	Ile	Phe	Leu	Leu	Val	Phe	Ser	Cys
		100					105					110			
Leu	Val	Leu	Ser	Val	Leu	Ser	Thr	Ile	Gln	Glu	His	Gln	Glu	Leu	Ala
		115				120					125				
Asn	Glu	Cys	Leu	Leu	Ile	Leu	Glu	Phe	Val	Met	Ile	Val	Val	Phe	Gly
	130					135				140					
Leu	Glu	Tyr	Ile	Val	Arg	Val	Trp	Ser	Ala	Gly	Cys	Cys	Cys	Arg	Tyr

581	586	591
Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Phe Tyr Asp Val Lys Asp		
585	587	588
Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile		
588	591	593
Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly		
590	593	590
Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu		
595	600	605
Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys		
610	615	620
Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr		
625	630	635
Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln		
645	650	655
Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val		
660	665	670
Asp His Glu Asp Ile Ser Val Ser Ala Gln Thr Leu Ser Ile Ser Arg		
675	680	685
Ser Val Ser Thr Asn Met Asp		
690	695	

210 3

211 24

212 INA

213 Artificial Sequence

220

223 Description of Artificial Sequence: PCR Primer

400 3

cagcggtctc tgagcgcccc gaggc

24

211 4

211 24

212 INA

213 Artificial Sequence

220

223 Description of Artificial Sequence: PCR Primer

400 4

aggcaggtc tgcgcgggga aaag

24

<210> 3
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 5
cagccacagag ctgtaactcc agg 23

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 6
aacctgctct ctgagccatg g 21

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 7
actgggtccg cgctgtgacc 20

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 8
ggctctccagg gtcagagtcg 20

<211> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<221>
<223> Description of Artificial Sequence: PCR Primer

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<210> 10
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 10
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21

<210> 11
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 11
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21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 12
agtcacgatg ggcagacctc g

21

<210> 12
<211> 11
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 13
ctctatgata aggtacctac c

11

<210> 14
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 14
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19

<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 15
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20

<210> 16
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 16
acacagggtt gacacacc

18

<210> 17
<211> 21
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 17
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<210> 18
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<220>
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<400> 18
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21

<210> 19
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<220>
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<400> 19
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<210> 20
<211> 21
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<213> Artificial Sequence

<220>
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<211> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 21
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<210> 22
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 22
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<210> 23
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<212> RNA
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<220>
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<400> 23
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<210> 24
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<212> RNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 24
ctcctgacct caagtgatec

20

<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<401> 25
gatagcacag agatggagag g

21

<210> 26
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<401> 26
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21

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PCR Primer

<401> 17
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21

<210> 28
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<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<401> 28
aacgcatact ccccatgtca

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<210> 21
<211> 21
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 23
tttggtttc ccagataaga

23

<210> 30
<211> 24
<212> DNA
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<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 30
tgtgaggag tgagttcaag tacg

24

<210> 31
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

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<210> 32
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<411> 33
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 <411> Homo sapiens

<411> 33

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Trp Gly Arg Leu Pro Gly Ala Arg Arg Gly Ser Ala Gly Leu Ala Lys
 20 25 30

Lys Cys Pro Phe Ser Leu Glu Leu Ala Glu Gly Gly Pro Ala Gly Gly
 35 40 45

Ala Leu Tyr Ala Pro Ile Ala Pro Gly Ala Pro Gly Pro Ala Pro Pro
 50 55 60

Ala Ser Pro Ala Ala Pro Ala Ala Pro Pro Val Ala Ser Asp Leu Gly
 65 70 75 80

Pro Arg Pro Pro Val Ser Leu Asp Pro Arg Val Ser Ile Tyr Ser Thr
 85 90 95

Arg Arg Pro Val Leu Ala Arg Thr His Val Gln Gly Arg Val Tyr Asn
 100 105 110

Phe Leu Glu Arg Pro Thr Gly Trp Lys Cys Phe Val Tyr His Phe Ala
 115 120 125

Val Phe Leu Ile Val Leu Val Cys Leu Ile Phe Ser Val Leu Ser Thr
 130 135 140

Ile Glu Gln Tyr Ala Ala Leu Ala Thr Gly Thr Leu Phe Trp Met Glu
 145 150 155 160

Ile Val Leu Val Val Phe Phe Gly Thr Glu Tyr Val Val Arg Leu Trp
 165 170 175

Ser Ala Gly Cys Arg Ser Lys Tyr Val Gly Leu Trp Gly Arg Leu Arg
 180 185 190

Phe Ala Arg Lys Pro Ile Ser Ile Ile Asp Leu Ile Val Val Val Ala
 195 200 205

Ser Met Val Val Leu Cys Val Gly Ser Lys Gly Gln Val Phe Ala Thr
 210 215 220

Ser Ala Ile Arg Gly Ile Arg Ile Leu Gln Ile Leu Arg Met Leu His
 235 240 245 250

Val Asp Arg Gln Gly Gly Thr Trp Arg Leu Leu Gly Ser Val Val Phe
 255 260 265

Ile His Arg Gln Glu Leu Ile Thr Thr Leu Tyr Ile Gly Phe Leu Gly
 270 275 280

Leu Ile Phe Ser Ser Tyr Phe Val Tyr Leu Ala Glu Lys Asp Ala Val
 285 290 295

Asn Glu Ser Gly Arg Val Glu Phe Gly Ser Tyr Ala Asp Ala Leu Trp
 300 305

Trp Gly Val Val Thr Val Thr Thr Ile Gly Tyr Gly Asp Lys Val Pro
 310 315 320

Gln Thr Trp Val Gly Lys Thr Ile Ala Ser Cys Phe Ser Val Phe Ala
 325 330 335

Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala
 340 345 350

Leu Lys Val Gln Gln Lys Gln Arg Gln Lys His Phe Asn Arg Gln Ile
 355 360 365

Pro Ala Ala Ala Ser Leu Ile Gln Thr Ala Trp Arg Cys Tyr Ala Ala
 370 375 380

Glu Asn Pro Asp Ser Ser Thr Trp Lys Ile Tyr Ile Arg Lys Ala Pro
 385 390 395 400

Arg Ser His Thr Leu Leu Ser Pro Ser Pro Lys Pro Lys Lys Ser Val
 405 410 415

Val Val Lys Lys Lys Lys Phe Lys Leu Asp Lys Asp Asn Gly Val Thr
 420 425 430

Pro Gly Glu Lys Met Leu Thr Val Pro His Ile Thr Cys Asp Pro Pro
 435 440 445

Glu Glu Arg Arg Leu Asp His Phe Ser Val Asp Gly Tyr Asp Ser Ser
 450 455 460

Val Arg Lys Ser Pro Thr Leu Leu Glu Val Ser Met Pro His Phe Met
 465 470 475 480

Arg Thr Asn Ser His Ala His Asp Leu Asp Leu His Gly His Thr Leu
470 480 490

Leu Thr Pro Ile Thr His Ile Ser Gln Leu Arg Gln His His Arg Ala
500 510 520

Thr Ile Lys Val Ile Arg Arg Met Gln Tyr Phe Val Ala Lys Lys Lys
530 540 550

Phe Gln Gln Ala Arg Lys Pro Tyr Asp Val Arg Asp Val Ile Gln Gln
560 570 580

Tyr Ser Gln Gly His Leu Asn Leu Met Val Arg Ile Lys Glu Leu Gln
590 600 610

Arg Arg Leu Asp Gln Ser Ile Gly Lys Pro Ser Leu Phe Ile Ser Val
620 630 640

Ser Glu Lys Ser Lys Asp Arg Gly Ser Asn Thr Ile Gly Ala Arg Leu
650 660 670

Asn Arg Val Glu Asp Lys Val Thr Gln Leu Asp Gln Arg Leu Ala Leu
680 690 700

Ile Thr Asp Met Leu His Gln Leu Leu Ser Leu His Gly Gly Ser Thr
710 720 730

Pro Gly Ser Gly Gly Pro Pro Arg Glu Gly Gly Ala His Ile Thr Gln
740 750 760

Pro Cys Gly Ser Gly Gly Ser Val Asp Pro Glu Leu Phe Leu Pro Ser
770 780 790

Asn Thr Leu Pro Thr Tyr Glu Gln Leu Thr Val Pro Arg Arg Gly Pro
800 810 820

Asp Glu Gly Ser
830

<210> 34

<211> 844

<212> PRT

<213> Homo sapiens

<400> 34

Met Val Gln Lys Ser Arg Asn Gly Gly Val Tyr Pro Gly Pro Ser Gly
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 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Gln Ala Pro
 35 41 45
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 51 55 61
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 65 70 75 80
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
 100 105 110
 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125
 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
 130 135 140
 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160
 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175
 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
 195 200 205
 Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
 210 215 220
 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
 225 230 235 240
 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
 245 250 255
 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 260 265 270

Ile Thr Leu Thr Thr Ile Gly Tyr Arg Asp Lys Tyr Pro Ala Thr Trp
 275 281 286

Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 291 296 301

Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 313 318 321

Gln Gln Gln His Arg Gln Lys His Phe Gln Lys Arg Arg Asn Pro Ala
 325 331 336

Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 340 345 350

Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
 355 360 365

Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
 370 375 380

Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
 385 390 395 400

Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
 405 410 415

Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala
 420 425 430

Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
 435 440 445

Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
 450 455 460

Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
 465 470 475 480

Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
 485 490 495

Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
 500 505 510

Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
 515 520 525

Ala Ser Leu Arg Pro Tyr Asp Val Met Asp Val Ile Gln Gln Tyr Ser
 581 585 591

Ala Gly His Leu Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg
 595 599 605 611

Val Asp Gln Ile Val Gly Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg
 615 621 627 633

Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Glu Asp Pro Ser Met Met
 639 645 651 657

Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys
 655 661 667 673

Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro
 675 681 687 693

Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro
 695 701 707 713 719

Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly
 721 727 733 739 745 751

Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn
 753 759 765 771 777 783

Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr
 785 791 797 803 809 815

Ser Trp Gln Pro Gln Ser His Pro Arg Gln Gly His Gly Thr Ser Pro
 821 827 833 839 845 851 857

Val Gly Asp His Gly Ser Leu Val Arg Ile Pro Pro Pro Pro Ala His
 859 865 871 877 883 889 895

Glu Arg Ser Leu Ser Ala Tyr Gly Gly Gly Asn Arg Ala Ser Met Glu
 897 903 909 915 921 927 933 939

Phe Leu Arg Gln Glu Asp Thr Pro Gly Cys Arg Pro Pro Glu Gly Thr
 941 947 953 959 965 971 977 983

Leu Arg Asp Ser Asp Thr Ser Ile Ser Ile Pro Ser Val Asp His Glu
 985 991 997 1003 1009 1015 1021 1027

Glu Leu Glu Arg Ser Phe Ser Gly Phe Ser Ile Ser Gln Ser Lys Glu
 1029 1035 1041 1047 1053 1059 1065 1071

Asn Leu Asp Ala Leu Asn Ser Cys Tyr Ala Ala Val Ala Pro Cys Ala
 71 74 77 80

Lys Val Arg Pro Tyr Ile Ala Glu Gly Glu Ser Asp Thr Asp Ser Asp
 81 84 87 90

Leu Cys Thr Pro Cys Gly Pro Pro Pro Arg Ser Ala Thr Gly Glu Gly
 91 94 97 100

Pro Phe Gly Asp Val Gly Trp Ala Gly Pro Arg Lys
 101 104

4210: 35

4211: 872

4212: PRT

4213: Homo sapiens

4400: 35

Met Gly Leu Lys Ala Arg Arg Ala Ala Gly Ala Ala Gly Gly Gly Gly
 1 5 10 15

Asp Gly Gly Gly Gly Gly Gly Gly Ala Ala Asn Pro Ala Gly Gly Asp
 20 25 30

Ala Ala Ala Ala Gly Asp Glu Glu Arg Lys Val Gly Leu Ala Pro Gly
 35 40 45

Asp Val Glu Gln Val Thr Leu Ala Leu Gly Ala Gly Ala Asp Lys Asp
 50 55 60

Gly Thr Leu Leu Leu Glu Gly Gly Gly Arg Asp Glu Gly Gln Arg Arg
 65 70 75 80

Thr Pro Gln Gly Ile Gly Leu Leu Ala Lys Thr Pro Leu Ser Arg Pro
 85 90 95

Val Lys Arg Asn Asn Ala Lys Tyr Arg Arg Ile Gln Thr Leu Ile Tyr
 100 105 110

Asp Ala Leu Glu Arg Pro Arg Gly Trp Ala Leu Leu Tyr His Ala Leu
 115 120 125

Val Phe Leu Ile Val Leu Gly Cys Leu Ile Leu Ala Val Leu Thr Thr
 130 135 140

Phe Lys Glu Tyr Glu Thr Val Ser Gly Asp Trp Leu Leu Leu Leu Glu

140															
Thr	Phe	Ala	Ile	Ile	Ile	Ile	Gly	Ala	Gln	Phe	Ala	Leu	Arg	Ile	Trp
			165						170						175
Ala	Ala	Gly	Cys	Cys	Cys	Arg	Tyr	Lys	Gly	Trp	Arg	Gly	Arg	Leu	Lys
			180					185						190	
Phe	Ala	Arg	Lys	Pro	Leu	Cys	Met	Leu	Asp	Ile	Phe	Val	Leu	Ile	Ala
			195				200						205		
Ser	Val	Pro	Val	Val	Ala	Val	Gly	Asn	Gln	Gly	Asn	Val	Leu	Ala	Thr
			210				215				220				
Ser	Leu	Arg	Ser	Leu	Arg	Phe	Leu	Gln	Ile	Leu	Arg	Met	Leu	Arg	Met
			225				230				235				240
Asp	Arg	Arg	Gly	Gly	Thr	Trp	Lys	Leu	Leu	Gly	Ser	Ala	Ile	Cys	Ala
			245						250					255	
His	Ser	Lys	Glu	Leu	Ile	Thr	Ala	Trp	Tyr	Ile	Gly	Phe	Leu	Thr	Leu
			260					265						270	
Ile	Leu	Ser	Ser	Phe	Leu	Val	Tyr	Leu	Val	Glu	Lys	Asp	Val	Pro	Glu
			275				280					285			
Val	Asp	Ala	Gln	Gly	Glu	Glu	Met	Lys	Glu	Glu	Phe	Glu	Thr	Tyr	Ala
			290				295					300			
Asp	Ala	Leu	Trp	Trp	Gly	Leu	Ile	Thr	Leu	Ala	Thr	Ile	Gly	Tyr	Gly
			305				310				315				320
Asp	Lys	Thr	Pro	Lys	Thr	Trp	Glu	Gly	Arg	Leu	Ile	Ala	Ala	Thr	Phe
			325						330					335	
Ser	Leu	Ile	Gly	Val	Ser	Phe	Phe	Ala	Leu	Pro	Ala	Gly	Ile	Leu	Gly
			340					345						350	
Ser	Gly	Leu	Ala	Leu	Lys	Val	Gln	Glu	Gln	His	Arg	Gln	Lys	His	Phe
			355				360					365			
Glu	Lys	Arg	Arg	Lys	Pro	Ala	Ala	Glu	Leu	Ile	Gln	Ala	Ala	Trp	Arg
			370				375				380				
Tyr	Tyr	Ala	Thr	Asn	Pro	Asn	Arg	Ile	Asp	Leu	Val	Ala	Thr	Trp	Arg
			385				390				395				400
Phe	Tyr	Glu	Ser	Val	Val	Ser	Phe	Pro	Phe	Phe	Arg	Lys	Glu	Gln	Leu

410 415 420
 Glu Ala Ala Ser Ser Glu Lys Leu Gly Leu Leu Asp Arg Val Arg Leu
 420 430 435
 Ser Asn Pro Arg Gly Ser Asn Thr Lys Gly Lys Leu Phe Thr Pro Leu
 435 440 445
 Asn Val Asp Ala Ile Glu Glu Ser Pro Ser Lys Glu Pro Lys Pro Val
 450 455 460
 Gly Leu Asn Asn Lys Glu Arg Phe Arg Thr Ala Phe Arg Met Lys Ala
 465 470 475 480
 Tyr Ala Phe Trp Gln Ser Ser Glu Asp Ala Gly Thr Gly Asp Pro Met
 485 490 495
 Ala Glu Asp Arg Gly Tyr Gly Asn Asp Phe Pro Ile Glu Asp Met Ile
 500 505 510
 Pro Thr Leu Lys Ala Ala Ile Arg Ala Val Arg Ile Leu Gln Phe Arg
 515 520 525
 Leu Tyr Lys Lys Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys
 530 535 540
 Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Ser Arg
 545 550 555 560
 Ile Lys Tyr Leu Gln Thr Arg Ile Asp Met Ile Phe Thr Pro Gly Pro
 565 570 575
 Pro Ser Thr Pro Lys His Lys Lys Ser Gln Lys Gly Ser Ala Phe Thr
 580 585 590
 Phe Pro Ser Gln Gln Ser Pro Arg Asn Glu Pro Tyr Val Ala Arg Pro
 595 600 605
 Ser Thr Ser Glu Ile Glu Asp Gln Ser Met Met Gly Lys Phe Val Lys
 610 615 620
 Val Glu Arg Gln Val Gln Asp Met Gly Lys Lys Leu Asp Phe Leu Val
 625 630 635 640
 Asp Met His Met Gln His Met Glu Arg Leu Gln Val Gln Val Thr Glu
 645 650 655
 Tyr Tyr Pro Thr Lys Gly Thr Ser Ser Pro Ala Glu Ala Glu Lys Lys

Glu Asp Asn Arg Tyr Ser Asp Leu Lys Thr Ile Ile Lys Asn Tyr Ser
678 681 685

Glu Thr Gly Pro Pro Glu Pro Pro Tyr Ser Phe His Glu Val Thr Ile
691 695 707

Asp Lys Val Ser Pro Tyr Gly Phe Phe Ala His Asp Pro Val Asn Leu
713 716 718 721

Pro Arg Gly Gly Pro Ser Ser Gly Lys Val Gln Ala Thr Pro Pro Ser
725 730 735

Ser Ala Thr Thr Tyr Val Glu Arg Pro Thr Val Leu Pro Ile Leu Thr
740 745 750

Leu Leu Asp Ser Arg Val Ser Cys His Ser Gln Ala Asp Leu Gln Gly
755 760 765

Pro Tyr Ser Asp Arg Ile Ser Pro Arg Gln Arg Arg Ser Ile Thr Arg
770 775 780

Asp Ser Asp Thr Pro Leu Ser Leu Met Ser Val Asn His Glu Glu Leu
785 790 795 800

Glu Arg Ser Pro Ser Gly Phe Ser Ile Ser Gln Asp Arg Asp Asp Tyr
805 810 815

Val Phe Gly Pro Asn Gly Gly Ser Ser Trp Met Arg Glu Lys Arg Tyr
821 825 830

Leu Ala Glu Gly Glu Thr Asp Thr Asp Thr Asp Pro Phe Thr Pro Ser
835 840 845

Gly Ser Met Pro Leu Ser Ser Thr Gly Asp Gly Ile Ser Asp Ser Val
850 855 860

Trp Thr Pro Ser Asn Lys Pro Ile
865 870

(210): 36

(211): 21

(212): DNA

(213): Artificial Sequence

(220):

<210> Description of Artificial Sequence: PCR Primer

<400> 36

aaggttggat cagtcattg g

21

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 37

aggttggcag gctgttgctg g

21

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 38

gacatggcac ctcccccgctg g

21

<210> 39

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 39

ccctctcaca tgtagggcct gac

23

<210> 40

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<217> Description of Artificial Sequence: PCR Primer

<217> 41

ccacgggaatg aacatatagt agac

24

<218> 41

<218> 24

<218> DNA

<218> Artificial Sequence

<219>

<223> Description of Artificial Sequence: PCR Primer

<400> 41

cagaagagtc aagatgggca ggac

24